

U9/744852

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SEQUENCE LISTING

<110> FROHBERG, Claus

<120> NUCLEIC ACID MOLECULES ENCODING β -AMYLASE, PLANTS WHICH SYNTHESIZE A MODIFIED STARCH, GENERATION PROCESSES AND USES

<130> 514413-3864

<150> PCT/EP99/05523

<151> 1999-07-30

<150> 198 36 099.1

<151> 1998-07-31

<160> 2

<170> PatentIn version 3.0

<210> 1

<211> 1950

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (16)..(1752)

<223> coding sequence beta-amylase

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Met Ala Met Ser Leu Pro His Gln Ile Gly Ala Leu
1 5 10

51

tca gga aca tcg ctc acg gcg gaa acc ggt gga gtt tca tgc gaa gtt
Ser Gly Thr Ser Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val
15 20 25

99

ccg gcg aag ggg agt tca gct aca tca gct atg tgg aga aca ccg atg
Pro Ala Lys Gly Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met
30 35 40

147

acg aat tta aaa gta tcg gta caa aaa aca gga act gaa att gac agg
Thr Asn Leu Lys Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg
45 50 55 60

195

gtg tcg ccg tcg ccg tcg ccg atg agt ccg atg atg gga gga gga
Val Ser Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly
65 70 75

243

atg cgg ccg gat tta tta gcg tgt caa gcg ttg atg gaa gct cag gta
Met Arg Pro Asp Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val
80 85 90

291

gat gag gta gtt gag aga gaa tat aag gtt agg aat tcg tcg gag aaa
Asp Glu Val Val Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys

339

95	100	105	
gag aaa gga gtt ccg gtg ttt gtt atg atg ccg ttg gat agt gtg aaa Glu Lys Gly Val Pro Val Phe Val Met Met Pro Leu Asp Ser Val Lys 110	115	120	387
atg gat cat act gtg aat agg aag aag gcg atg aat gcg agt tta cag Met Asp His Thr Val Asn Arg Lys Lys Ala Met Asn Ala Ser Leu Gln 125	130	135	435
gcg ttg aag agc gcc ggt gtg gaa ggg att atg atg gat gtg tgg tgg Ala Leu Lys Ser Ala Gly Val Glu Gly Ile Met Met Asp Val Trp Trp 145	150	155	483
gga ttg gtg gag aga gat gcg ccg gga gag tat aat tgg ggc ggt tat Gly Leu Val Glu Arg Asp Ala Pro Gly Glu Tyr Asn Trp Gly Gly Tyr 160	165	170	531
gct gag ctt atg gaa atg gcg aaa aaa cat gga ctc aaa gtt caa gct Ala Glu Leu Met Glu Met Ala Lys Lys His Gly Leu Lys Val Gln Ala 175	180	185	579
gtg atg tct ttc cat caa tgt ggt gga aac gtc ggt gat tcc tgc acg Val Met Ser Phe His Gln Cys Gly Gly Asn Val Gly Asp Ser Cys Thr 190	195	200	627
atc cct ctt cca agg tgg gtt gag gag atg gag aag gat cca gat Ile Pro Leu Pro Arg Trp Val Val Glu Glu Met Glu Lys Asp Pro Asp 205	210	215	675
ctt gca tac aca gat cag tgg gga agg agg aat ttt gaa tat gta tcg Leu Ala Tyr Thr Asp Gln Trp Gly Arg Arg Asn Phe Glu Tyr Val Ser 225	230	235	723
ctt ggt tgc gat aca ctt cca gtt ctt aaa gga agg act cct gtc caa Leu Gly Cys Asp Thr Leu Pro Val Leu Lys Gly Arg Thr Pro Val Gln 240	245	250	771
tgc tat tct gat ttc atg aga ggg ttt aga gat aga ttt gag aat ctc Cys Tyr Ser Asp Phe Met Arg Gly Phe Arg Asp Arg Phe Glu Asn Leu 255	260	265	819
cta ggt gac acc att gtg gaa att caa gtc ggg atg ggt cca gct gga Leu Gly Asp Thr Ile Val Glu Ile Gln Val Gly Met Gly Pro Ala Gly 270	275	280	867
gag ctc cgt tat cca tcc tat ccg gaa aaa gat gga gta tgg aaa ttc Glu Leu Arg Tyr Pro Ser Tyr Pro Glu Lys Asp Gly Val Trp Lys Phe 285	290	295	915
cct gga att ggt gct ttt cag tgt tat gac aag tac atg atc agt agc Pro Gly Ile Gly Ala Phe Gln Cys Tyr Asp Lys Tyr Met Ile Ser Ser 305	310	315	963
tta cag ggt gca gca gaa gct ttt ggt aag cct gaa tgg gga cac acc Leu Gln Gly Ala Ala Glu Ala Phe Gly Lys Pro Glu Trp Gly His Thr 320	325	330	1011

ggt cca acc gat gct ggt cag tac aac aat tgg cca gaa gat acc aac Gly Pro Thr Asp Ala Gly Gln Tyr Asn Asn Trp Pro Glu Asp Thr Asn 335 340 345	1059
ttt ttc aag aag gaa ggt ggt gga tgg gat agt caa tat ggg gag ttc Phe Phe Lys Lys Glu Gly Gly Trp Asp Ser Gln Tyr Gly Glu Phe 350 355 360	1107
ttc ctc act tgg tat tct gag atg ctt ttg aac cat ggt gag agg ata Phe Leu Thr Trp Tyr Ser Glu Met Leu Leu Asn His Gly Glu Arg Ile 365 370 375 380	1155
ctg caa tca gcc aag gcg ata ttc gag gac aag ggt gtt aag att tca Leu Gln Ser Ala Lys Ala Ile Phe Glu Asp Lys Gly Val Lys Ile Ser 385 390 395	1203
gtt aag att gca ggt att cac tgg cac tat gga aca agg tcc cat gcc Val Lys Ile Ala Gly Ile His Trp His Tyr Gly Thr Arg Ser His Ala 400 405 410	1251
cct gag ctg acc gct gga tac tac aac acc cgt aac cga gat ggt tac Pro Glu Leu Thr Ala Gly Tyr Tyr Asn Thr Arg Asn Arg Asp Gly Tyr 415 420 425	1299
ctt ccc atc gcc caa atg ctt gcc cgc cac ggt gca gtt ttc aac ttc Leu Pro Ile Ala Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe 430 435 440	1347
aca tgt gtt gag atg cgt gac cac gag cag cca caa gat gca cta tgt Thr Cys Val Glu Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys 445 450 455 460	1395
gca cct gag aag ttg gtt agg caa gtg gct tta gca act cag gaa gct Ala Pro Glu Lys Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala 465 470 475	1443
caa gtt cca ctt gct ggg gag aat gca ttg cca cga tac gat gat tat Gln Val Pro Leu Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr 480 485 490	1491
gca cat gaa cag atc ctt caa gca tcc tca ttg aat atc aac gat caa Ala His Glu Gln Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln 495 500 505	1539
tca ggt gat aga gag atg tgc gcg ttt aca tat ttg agg atg aat cct Ser Gly Asp Arg Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro 510 515 520	1587
gac cta ttc cat cct gat aac tgg agg cga ttc gtt gcc ttc gtg aag Asp Leu Phe His Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys 525 530 535 540	1635
aaa atg aaa gaa gga aaa gac gca aac aaa tgc cgg gaa caa gta gag Lys Met Lys Glu Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu 545 550 555	1683

agg gag gca gag cat ttc gtg cat ata act cag ccg tta gtg caa gaa , 1731
Arg Glu Ala Glu His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu
560 565 570

gct gca gct gcc ctc atg cac taagcaaatg gttgtcaaat agtactgtaa 1782
Ala Ala Ala Ala Leu Met His
575

ttttgatcct tttagctaac atggagtttt tcaacatgtt acgaggatct tatagctcgt 1842
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tatgtcttaa tgaaatgata cataattcag tagaaaaaaaaaaaaaaaaa 1950

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<211> 579
<212> PRT
<213> Solanum tuberosum

<400> 2

Met Ala Met Ser Leu Pro His Gln Ile Gly Ala Leu Ser Gly Thr Ser
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Leu Thr Ala Glu Thr Gly Gly Val Ser Cys Glu Val Pro Ala Lys Gly
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Ser Ser Ala Thr Ser Ala Met Trp Arg Thr Pro Met Thr Asn Leu Lys
35 40 45

Val Ser Val Gln Lys Thr Gly Thr Glu Ile Asp Arg Val Ser Pro Ser
50 55 60

Pro Ser Pro Pro Met Ser Pro Met Met Gly Gly Gly Met Arg Pro Asp
65 70 75 80

Leu Leu Ala Cys Gln Ala Leu Met Glu Ala Gln Val Asp Glu Val Val
85 90 95

Glu Arg Glu Tyr Lys Val Arg Asn Ser Ser Glu Lys Glu Lys Gly Val
100 105 110

Pro Val Phe Val Met Met Pro Leu Asp Ser Val Lys Met Asp His Thr
115 120 125

Val Asn Arg Lys Lys Ala Met Asn Ala Ser Leu Gln Ala Leu Lys Ser
130 135 140

Ala Gly Val Glu Gly Ile Met Met Asp Val Trp Trp Gly Leu Val Glu
145 150 155 160

Arg Asp Ala Pro Gly Glu Tyr Asn Trp Gly Gly Tyr Ala Glu Leu Met
165 170 175

Glu Met Ala Lys Lys His Gly Leu Lys Val Gln Ala Val Met Ser Phe
180 185 190

His Gln Cys Gly Gly Asn Val Gly Asp Ser Cys Thr Ile Pro Leu Pro
195 200 205

Arg Trp Val Val Glu Glu Met Glu Lys Asp Pro Asp Leu Ala Tyr Thr
210 215 220

Asp Gln Trp Gly Arg Arg Asn Phe Glu Tyr Val Ser Leu Gly Cys Asp
225 230 235 240

Thr Leu Pro Val Leu Lys Gly Arg Thr Pro Val Gln Cys Tyr Ser Asp
245 250 255

Phe Met Arg Gly Phe Arg Asp Arg Phe Glu Asn Leu Leu Gly Asp Thr
260 265 270

Ile Val Glu Ile Gln Val Gly Met Gly Pro Ala Gly Glu Leu Arg Tyr
275 280 285

Pro Ser Tyr Pro Glu Lys Asp Gly Val Trp Lys Phe Pro Gly Ile Gly
290 295 300

Ala Phe Gln Cys Tyr Asp Lys Tyr Met Ile Ser Ser Leu Gln Gly Ala
305 310 315 320

Ala Glu Ala Phe Gly Lys Pro Glu Trp Gly His Thr Gly Pro Thr Asp
325 330 335

Ala Gly Gln Tyr Asn Asn Trp Pro Glu Asp Thr Asn Phe Phe Lys Lys
340 345 350

Glu Gly Gly Trp Asp Ser Gln Tyr Gly Glu Phe Phe Leu Thr Trp
355 360 365

Tyr Ser Glu Met Leu Leu Asn His Gly Glu Arg Ile Leu Gln Ser Ala
370 375 380

Lys Ala Ile Phe Glu Asp Lys Gly Val Lys Ile Ser Val Lys Ile Ala
385 390 395 400

Gly Ile His Trp His Tyr Gly Thr Arg Ser His Ala Pro Glu Leu Thr
405 410 415

Ala Gly Tyr Tyr Asn Thr Arg Asn Arg Asp Gly Tyr Leu Pro Ile Ala
420 425 430

Gln Met Leu Ala Arg His Gly Ala Val Phe Asn Phe Thr Cys Val Glu
435 440 445

Met Arg Asp His Glu Gln Pro Gln Asp Ala Leu Cys Ala Pro Glu Lys
450 455 460

Leu Val Arg Gln Val Ala Leu Ala Thr Gln Glu Ala Gln Val Pro Leu
465 470 475 480

Ala Gly Glu Asn Ala Leu Pro Arg Tyr Asp Asp Tyr Ala His Glu Gln
485 490 495

Ile Leu Gln Ala Ser Ser Leu Asn Ile Asn Asp Gln Ser Gly Asp Arg
500 505 510

Glu Met Cys Ala Phe Thr Tyr Leu Arg Met Asn Pro Asp Leu Phe His
515 520 525

Pro Asp Asn Trp Arg Arg Phe Val Ala Phe Val Lys Lys Met Lys Glu
530 535 540

Gly Lys Asp Ala Asn Lys Cys Arg Glu Gln Val Glu Arg Glu Ala Glu
545 550 555 560

His Phe Val His Ile Thr Gln Pro Leu Val Gln Glu Ala Ala Ala Ala
565 570 575

Leu Met His